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- Search numbers may not be continuous; all searches are represented.
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<a href="#">#13</a>	Search #6 and #7 Limits: Publication Date from 1965 to 1999	11:33:59	<a href="#">288</a>
<a href="#">#12</a>	Search #6 and #7 Sort by: PublicationDate	11:27:26	<a href="#">540</a>
<a href="#">#11</a>	Search #10 and #6	11:26:41	<a href="#">467</a>
<a href="#">#10</a>	Search pain	11:25:46	<a href="#">331999</a>
<a href="#">#8</a>	Search #5 and #6 and #7 Sort by: PublicationDate	11:03:38	<a href="#">26</a>
<a href="#">#7</a>	Search drug development	11:03:08	<a href="#">234051</a>
<a href="#">#6</a>	Search sodium channel	11:02:59	<a href="#">11764</a>
<a href="#">#5</a>	Search epilepsy	11:02:50	<a href="#">101439</a>
<a href="#">#4</a>	Search epliepsy	11:02:44	<a href="#">1</a>
<a href="#">#3</a>	Search scn1a AND epilepsy	11:02:28	<a href="#">110</a>
<a href="#">#2</a>	Search scn1a	10:56:10	<a href="#">131</a>
<a href="#">#1</a>	Search scn1a AND rat Sort by: PublicationDate	10:55:42	<a href="#">16</a>

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Aug 14 2006 08:07:58

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1790	(sodium adj channel)	USPAT; DERWENT	OR	ON	2006/08/16 11:10
L2	12794	epilepsy	USPAT; DERWENT	OR	ON	2006/08/16 11:10
L3	1892	(sodium adj channel) or scn1\$	USPAT; DERWENT	OR	ON	2006/08/16 11:11
L4	160859	screening	USPAT; DERWENT	OR	ON	2006/08/16 11:11
L5	160	I2 and I3 and I4	USPAT; DERWENT	OR	ON	2006/08/16 11:15
L6	3775	sodium and brain and voltage	USPAT; DERWENT	OR	ON	2006/08/16 11:16
L7	415	I6 and I2 and I4	USPAT; DERWENT	OR	ON	2006/08/16 11:17
L8	589	I6 and pain and I4	USPAT; DERWENT	OR	ON	2006/08/16 11:20
L9	430	I6 and pain and (screen\$ with assay)	USPAT; DERWENT	OR	ON	2006/08/16 11:20
S1	1	"10664423"	US-PGPUB; USPAT	OR	ON	2006/08/16 11:10
S2	60	scn1a	US-PGPUB; USPAT	OR	ON	2006/08/08 13:58
S3	3479	sodium adj channel\$	US-PGPUB; USPAT	OR	ON	2006/08/08 13:58
S4	66	scn1a	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/08 13:58
S5	4029	sodium adj channel\$	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/08 13:58
S6	56	S4 and S5	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/08 14:11
S7	2	"5223409".pn.	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/08 14:12
S8	3	"9921875"	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/08 14:57

## EAST Search History

S9	10	S4 not S6	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/08 14:57
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GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 07:22:25 ; Search time 4424 Seconds  
 (without alignments)  
 13203.774 Million cell updates/sec

Title: US-10-664-423A-1  
 Perfect score: 8378  
 Sequence: 1 tactgcagaggtctctggtg.....agattacattttttatttta 8378

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
 1: geneseqn1980s:\*  
 2: geneseqn1990s:\*  
 3: geneseqn2000s:\*  
 4: geneseqn2001as:\*  
 5: geneseqn2001bs:\*  
 6: geneseqn2002as:\*  
 7: geneseqn2002bs:\*  
 8: geneseqn2003as:\*  
 9: geneseqn2003bs:\*  
 10: geneseqn2003cs:\*  
 11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*  
 14: geneseqn2005s:\*  
 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	8378	100.0	8378	5	AAH55763	Aah55763 Human adu	
2	8336	99.5	8381	6	ABK98846	Abk98846 Human sod	
3	8334.4	99.5	8381	6	ABK98924	Abk98924 Human sod	
4	8332.8	99.5	8381	6	ABK98843	Abk98843 Human sod	
5	8332.8	99.5	8381	6	ABK98844	Abk98844 Human sod	
6	8332.8	99.5	8381	6	ABK98841	Abk98841 Human sod	
7	8332.8	99.5	8381	6	ABK98842	Abk98842 Human sod	

8	8332.8	99.5	8381	6	ABK98845	Abk98845 Human sod
9	8332.8	99.5	8381	6	ABK98847	Abk98847 Human sod
10	8332.8	99.5	8381	10	ADB78632	Adb78632 Human ion
11	8332.8	99.5	8381	10	ADB78634	Adb78634 Human ion
12	8332.8	99.5	8381	10	ADB78638	Adb78638 Human ion
13	8332.8	99.5	8381	10	ADB78633	Adb78633 Human ion
14	8332.8	99.5	8381	10	ADB78637	Adb78637 Human ion
15	8332.8	99.5	8381	10	ADB78649	Adb78649 Human ion
16	8332.8	99.5	8381	13	ADS87498	Ads87498 Mutant SC
17	8332.8	99.5	8381	13	ADS87479	Ads87479 Mutant SC
18	8332.8	99.5	8381	13	ADS87483	Ads87483 Mutant SC
19	8332.8	99.5	8381	13	ADS87477	Ads87477 Mutant SC
20	8332.8	99.5	8381	13	ADS87499	Ads87499 Mutant SC
21	8332.8	99.5	8381	13	ADS87480	Ads87480 Mutant SC
22	8332.8	99.5	8381	13	ADS87484	Ads87484 Mutant SC
23	8332.8	99.5	8381	13	ADS87525	Ads87525 Mutant SC
24	8332.8	99.5	8381	13	ADS87488	Ads87488 Mutant SC
25	8332.8	99.5	8381	13	ADS87526	Ads87526 Mutant SC
26	8332.8	99.5	8381	13	ADS87486	Ads87486 Mutant SC
27	8332.8	99.5	8381	13	ADS87482	Ads87482 Mutant SC
28	8332.8	99.5	8381	13	ADS87490	Ads87490 Mutant SC
29	8332.8	99.5	8381	13	ADS87481	Ads87481 Mutant SC
30	8332.8	99.5	8381	13	ADS87489	Ads87489 Mutant SC
31	8332.8	99.5	8381	13	ADS87527	Ads87527 Mutant SC
32	8332.8	99.5	8381	13	ADS87485	Ads87485 Mutant SC
33	8332.8	99.5	8381	13	ADS87487	Ads87487 Mutant SC
34	8332.8	99.5	8381	13	ADS87478	Ads87478 Mutant SC
35	8332.8	99.5	8381	14	ADY27073	Ady27073 Human SCN
36	8332.8	99.5	8381	14	ADY27068	Ady27068 Human SCN
37	8332.8	99.5	8381	14	ADY27072	Ady27072 Human SCN
38	8332.8	99.5	8381	14	ADY27070	Ady27070 Human SCN
39	8332.8	99.5	8381	14	ADY27071	Ady27071 Human SCN
40	8332.8	99.5	8381	14	ADY27067	Ady27067 Human SCN
41	8332.8	99.5	8381	14	ADY27065	Ady27065 Human SCN
42	8332.8	99.5	8381	14	ADY27066	Ady27066 Human SCN
43	8332.8	99.5	8381	14	ADY27069	Ady27069 Human SCN
44	8322.4	99.3	8380	10	ADB78630	Adb78630 Human ion
45	8322.4	99.3	8380	13	ADS87496	Ads87496 Mutant SC

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2006, 21:17:02 ; Search time 30172 Seconds  
 (without alignments)  
 17756.579 Million cell updates/sec

Title: US-10-664-423A-1  
 Perfect score: 8378  
 Sequence: 1 tactgcagaggtctctggtg.....agattacattttttatttta 8378

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : GenEmbl:\*  
 1: gb\_env:\*  
 2: gb\_pat:\*  
 3: gb\_ph:\*  
 4: gb\_pl:\*  
 5: gb\_pr:\*  
 6: gb\_ro:\*  
 7: gb\_sts:\*  
 8: gb\_sy:\*  
 9: gb\_un:\*  
 10: gb\_vi:\*  
 11: gb\_ov:\*  
 12: gb\_htg:\*  
 13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	IDB	ID	Description
1	8378	100.0	8378	2	AX164171	AX164171 Sequence
2	8292	99.0	8378	2	AX164172	AX164172 Sequence
3	7952.4	94.9	8131	2	BD094360	BD094360 Sodium ch
4	7952.4	94.9	8131	2	BD105257	BD105257 Sodium ch
5	7952.4	94.9	8131	5	AF225985	AF225985 Homo sapi
6	6220	74.2	8398	6	RNSCPIR	X03638 Rat brain m
7	6209	74.1	8399	6	RATNACHI	M22253 Rattus norv

8	6016.4	71.8	6030	5	AB093548	AB093548 Homo sapi
9	6015.2	71.8	6030	2	AX391140	AX391140 Sequence
10	6003.6	71.7	6030	2	BD144093	BD144093 GEFS + re
11	5997.4	71.6	6027	2	AX709969	AX709969 Sequence
12	5960.8	71.1	6046	5	AY043484	AY043484 Homo sapi
13	5940.4	70.9	5997	5	AB093549	AB093549 Homo sapi
14	5939.2	70.9	5997	2	AX391130	AX391130 Sequence
15	5928.8	70.8	5997	2	DD182524	DD182524 Mutations
16	5902.2	70.4	5922	2	AX391142	AX391142 Sequence
17	5838.4	69.7	5946	5	AB098335	AB098335 Homo sapi
18	5826.2	69.5	5889	2	AX391132	AX391132 Sequence
19	4614.4	55.1	8292	2	AX805577	AX805577 Sequence
20	4591	54.8	8349	2	AX164203	AX164203 Sequence
21	4591	54.8	8349	2	AX164204	AX164204 Sequence
22	4323.2	51.6	4362	2	AX391144	AX391144 Sequence
23	4313.8	51.5	6328	5	HUMHBAX	M94055 Human volta
24	4247.2	50.7	4329	2	AX391134	AX391134 Sequence
25	4209.8	50.2	6018	2	BD144094	BD144094 GEFS + re
26	4205	50.2	9123	2	BD094361	BD094361 Sodium ch
27	4205	50.2	9123	2	BD105258	BD105258 Sodium ch
28	4205	50.2	9123	5	AF225987	AF225987 Homo sapi
29	4137.2	49.4	4179	2	AX391146	AX391146 Sequence
30	4061.2	48.5	4146	2	AX391136	AX391136 Sequence
31	4051.2	48.4	8553	6	RNSCPIIR	X03639 Rat brain m
32	4044.2	48.3	4197	2	AX391148	AX391148 Sequence
33	4040.8	48.2	8552	6	RATNACHII	M22254 Rattus norv
34	3968.2	47.4	4164	2	AX391138	AX391138 Sequence
35	3954.6	47.2	8378	11	AF123593	AF123593 Cynops py
36	3949.6	47.1	9112	2	AX164235	AX164235 Sequence
37	3947.8	47.1	8976	5	AF225986	AF225986 Homo sapi
38	3941.2	47.0	4809	2	CQ727958	CQ727958 Sequence
39	3922.4	46.8	9112	2	AX164236	AX164236 Sequence
40	3864	46.1	6599	5	HSA251507	AJ251507 Homo sapi
41	3641	43.5	6822	2	AX401928	AX401928 Sequence
42	3641	43.5	6822	6	RNSCIII	Y00766 Rat mRNA fo
43	3576.8	42.7	6404	2	AR107906	AR107906 Sequence
44	3576.8	42.7	6404	2	AR483561	AR483561 Sequence
45	3508.8	41.9	6348	2	AR448089	AR448089 Sequence

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2006, 05:52:58 ; Search time 1369 Seconds  
 (without alignments)  
 11450.803 Million cell updates/sec

Title: US-10-664-423A-1  
 Perfect score: 8378  
 Sequence: 1 tactgcagaggtctctggtg.....agattacattttttatttta 8378

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4303	51.4	6332	3	US-09-949-016-5117	Sequence 5117, Ap
2	3576.8	42.7	6404	3	US-08-836-325-14	Sequence 14, Appl
3	3576.8	42.7	6404	3	US-09-457-571-14	Sequence 14, Appl
4	3508.8	41.9	6348	3	US-09-976-594-756	Sequence 756, App
5	3508.8	41.9	6348	3	US-09-919-039-366	Sequence 366, App
6	3508.8	41.9	6371	3	US-08-836-325-13	Sequence 13, Appl
7	3508.8	41.9	6371	3	US-09-457-571-13	Sequence 13, Appl
8	3418.6	40.8	6452	3	US-08-836-325-9	Sequence 9, Appli
9	3418.6	40.8	6452	3	US-09-457-571-9	Sequence 9, Appli
10	3183	38.0	5106	3	US-09-976-594-1104	Sequence 1104, Ap
11	2821	33.7	6882	3	US-09-949-016-4205	Sequence 4205, Ap
12	2779	33.2	6007	3	US-09-024-020B-2	Sequence 2, Appli



13	2779	33.2	6007	3	US-09-425-043-2	Sequence 2, Appli
14	2756.8	32.9	6586	3	US-09-024-020B-43	Sequence 43, Appl
15	2756.8	32.9	6586	3	US-09-425-043-43	Sequence 43, Appl
16	2737.4	32.7	6556	3	US-09-024-020B-7	Sequence 7, Appli
17	2737.4	32.7	6556	3	US-09-425-043-7	Sequence 7, Appli
18	2730.2	32.6	5977	3	US-09-024-020B-1	Sequence 1, Appli
19	2730.2	32.6	5977	3	US-09-425-043-1	Sequence 1, Appli
20	2661.8	31.8	6826	3	US-09-024-020B-8	Sequence 8, Appli
21	2661.8	31.8	6826	3	US-09-425-043-8	Sequence 8, Appli
22	2483.6	29.6	2490	3	US-09-976-594-361	Sequence 361, App
23	1894	22.6	6048	3	US-09-634-920-3	Sequence 3, Appli
24	1894	22.6	6048	3	US-09-514-907A-1	Sequence 1, Appli
25	1894	22.6	6048	3	US-09-896-994-1	Sequence 1, Appli
26	1894	22.6	6048	3	US-09-840-125-3	Sequence 3, Appli
27	1778.2	21.2	3033	3	US-08-836-325-1	Sequence 1, Appli
28	1778.2	21.2	3033	3	US-09-457-571-1	Sequence 1, Appli
29	1529.6	18.3	5874	3	US-08-843-417-9	Sequence 9, Appli
30	1529.6	18.3	5874	3	US-09-527-013-9	Sequence 9, Appli
31	1464.2	17.5	6527	3	US-08-669-656A-7	Sequence 7, Appli
32	1458.8	17.4	6524	3	US-08-669-656A-1	Sequence 1, Appli
33	1455.4	17.4	6344	3	US-08-843-417-1	Sequence 1, Appli
34	1455.4	17.4	6344	3	US-09-527-013-1	Sequence 1, Appli
35	1350.8	16.1	7052	3	US-08-669-656A-5	Sequence 5, Appli
36	1321.8	15.8	5482	3	US-09-920-653B-2	Sequence 2, Appli
37	1283.2	15.3	99830	3	US-09-949-016-16859	Sequence 16859, A
38	1092.6	13.0	5822	3	US-09-354-147C-4	Sequence 4, Appli
39	1080.2	12.9	5860	3	US-09-354-147C-41	Sequence 41, Appl
40	1077	12.9	5875	3	US-09-354-147C-1	Sequence 1, Appli
41	1035.4	12.4	6519	2	US-08-808-793-24	Sequence 24, Appl
42	977	11.7	5461	3	US-07-998-289B-7	Sequence 7, Appli
43	924.4	11.0	6318	2	US-08-808-793-1	Sequence 1, Appli
44	924.4	11.0	6318	3	US-08-772-512A-1	Sequence 1, Appli
45	924.4	11.0	6318	3	US-09-428-371-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2006, 06:32:27 ; Search time 6053 Seconds  
 (without alignments)  
 17007.403 Million cell updates/sec

Title: US-10-664-423A-1  
 Perfect score: 8378  
 Sequence: 1 tactgcagaggtctctggtg.....agattacattttttatttta 8378

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	8378	100.0	8378	US-10-664-422-1	Sequence 1, Appli
2	8378	100.0	8378	US-10-664-423-1	Sequence 1, Appli
3	8378	100.0	8378	US-10-664-603-1	Sequence 1, Appli
4	8336	99.5	8381	US-10-451-126A-9	Sequence 9, Appli
5	8334.4	99.5	8381	US-10-451-126A-89	Sequence 89, Appl
6	8332.8	99.5	8381	US-10-451-126A-1	Sequence 1, Appli

7	8332.8	99.5	8381	8	US-10-451-126A-3	Sequence 3, Appli
8	8332.8	99.5	8381	8	US-10-451-126A-5	Sequence 5, Appli
9	8332.8	99.5	8381	8	US-10-451-126A-7	Sequence 7, Appli
10	8332.8	99.5	8381	8	US-10-451-126A-8	Sequence 8, Appli
11	8332.8	99.5	8381	8	US-10-451-126A-11	Sequence 11, Appl
12	8332.8	99.5	8381	9	US-10-806-899-1	Sequence 1, Appli
13	8332.8	99.5	8381	9	US-10-806-899-2	Sequence 2, Appli
14	8332.8	99.5	8381	9	US-10-806-899-3	Sequence 3, Appli
15	8332.8	99.5	8381	9	US-10-806-899-4	Sequence 4, Appli
16	8332.8	99.5	8381	9	US-10-806-899-5	Sequence 5, Appli
17	8332.8	99.5	8381	9	US-10-806-899-6	Sequence 6, Appli
18	8332.8	99.5	8381	9	US-10-806-899-7	Sequence 7, Appli
19	8332.8	99.5	8381	9	US-10-806-899-8	Sequence 8, Appli
20	8332.8	99.5	8381	9	US-10-806-899-9	Sequence 9, Appli
21	8332.8	99.5	8381	9	US-10-806-899-10	Sequence 10, Appl
22	8332.8	99.5	8381	9	US-10-806-899-11	Sequence 11, Appl
23	8332.8	99.5	8381	9	US-10-806-899-12	Sequence 12, Appl
24	8332.8	99.5	8381	9	US-10-806-899-13	Sequence 13, Appl
25	8332.8	99.5	8381	9	US-10-806-899-14	Sequence 14, Appl
26	8332.8	99.5	8381	9	US-10-806-899-22	Sequence 22, Appl
27	8332.8	99.5	8381	9	US-10-806-899-23	Sequence 23, Appl
28	8332.8	99.5	8381	9	US-10-806-899-49	Sequence 49, Appl
29	8332.8	99.5	8381	9	US-10-806-899-50	Sequence 50, Appl
30	8332.8	99.5	8381	9	US-10-806-899-51	Sequence 51, Appl
31	8332.8	99.5	8381	10	US-10-482-834A-3	Sequence 3, Appli
32	8332.8	99.5	8381	10	US-10-482-834A-4	Sequence 4, Appli
33	8332.8	99.5	8381	10	US-10-482-834A-5	Sequence 5, Appli
34	8332.8	99.5	8381	10	US-10-482-834A-8	Sequence 8, Appli
35	8332.8	99.5	8381	10	US-10-482-834A-9	Sequence 9, Appli
36	8332.8	99.5	8381	10	US-10-482-834A-20	Sequence 20, Appl
37	8322.4	99.3	8380	9	US-10-806-899-15	Sequence 15, Appl
38	8322.4	99.3	8380	9	US-10-806-899-17	Sequence 17, Appl
39	8322.4	99.3	8380	9	US-10-806-899-18	Sequence 18, Appl
40	8322.4	99.3	8380	9	US-10-806-899-20	Sequence 20, Appl
41	8322.4	99.3	8380	9	US-10-806-899-21	Sequence 21, Appl
42	8322.4	99.3	8380	9	US-10-806-899-52	Sequence 52, Appl
43	8322.4	99.3	8380	10	US-10-482-834A-1	Sequence 1, Appli
44	8320.4	99.3	8379	9	US-10-806-899-19	Sequence 19, Appl
45	8320.4	99.3	8379	9	US-10-806-899-53	Sequence 53, Appl

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2006, 08:44:48 ; Search time 176 Seconds  
 (without alignments)  
 11411.446 Million cell updates/sec

Title: US-10-664-423A-1  
 Perfect score: 8378  
 Sequence: 1 tactgcagaggtctctggtg.....agattacattttttatttta 8378

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_NA\_New:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8336	99.5	8381	7	US-11-263-326-9	Sequence 9, Appli
2	8332.8	99.5	8381	7	US-11-263-326-1	Sequence 1, Appli
3	8332.8	99.5	8381	7	US-11-263-326-3	Sequence 3, Appli
4	8332.8	99.5	8381	7	US-11-263-326-5	Sequence 5, Appli
5	8332.8	99.5	8381	7	US-11-263-326-7	Sequence 7, Appli
6	8332.8	99.5	8381	7	US-11-263-326-8	Sequence 8, Appli
7	8332.8	99.5	8381	7	US-11-263-326-11	Sequence 11, Appl
8	8332.8	99.5	8381	7	US-11-263-326-91	Sequence 91, Appl
9	8332.8	99.5	8381	7	US-11-263-326-92	Sequence 92, Appl
10	8332.8	99.5	8381	7	US-11-263-326-93	Sequence 93, Appl
11	8332.8	99.5	8381	7	US-11-263-326-96	Sequence 96, Appl
12	8332.8	99.5	8381	7	US-11-263-326-97	Sequence 97, Appl
13	8332.8	99.5	8381	7	US-11-263-326-108	Sequence 108, App
14	8332.8	99.5	8381	7	US-11-263-326-136	Sequence 136, App

15	8332.8	99.5	8381	7	US-11-263-326-137	Sequence 137, App
16	8332.8	99.5	8381	7	US-11-263-326-138	Sequence 138, App
17	8332.8	99.5	8381	7	US-11-263-326-139	Sequence 139, App
18	8332.8	99.5	8381	7	US-11-263-326-140	Sequence 140, App
19	8332.8	99.5	8381	7	US-11-263-326-141	Sequence 141, App
20	8332.8	99.5	8381	7	US-11-263-326-142	Sequence 142, App
21	8332.8	99.5	8381	7	US-11-263-326-143	Sequence 143, App
22	8332.8	99.5	8381	7	US-11-263-326-144	Sequence 144, App
23	8322.4	99.3	8380	7	US-11-263-326-89	Sequence 89, Appl
24	8317.4	99.3	8388	7	US-11-263-326-94	Sequence 94, Appl
25	8316.4	99.3	8377	7	US-11-263-326-95	Sequence 95, Appl
26	8302.4	99.1	8370	7	US-11-263-326-90	Sequence 90, Appl
27	5928.8	70.8	5997	7	US-11-313-450-1	Sequence 1, Appli
28	4614.4	55.1	8292	6	US-10-501-814-2	Sequence 2, Appli
29	4315.4	51.5	6328	7	US-11-263-326-102	Sequence 102, App
30	4313.8	51.5	6328	7	US-11-263-326-101	Sequence 101, App
31	4313.8	51.5	6328	7	US-11-263-326-103	Sequence 103, App
32	4313.8	51.5	6328	7	US-11-263-326-146	Sequence 146, App
33	4313.8	51.5	6328	7	US-11-263-326-147	Sequence 147, App
34	4313.8	51.5	6328	7	US-11-263-326-148	Sequence 148, App
35	4313.8	51.5	6328	7	US-11-263-326-149	Sequence 149, App
36	4313.8	51.5	6328	7	US-11-263-326-150	Sequence 150, App
37	4313.8	51.5	6328	7	US-11-263-326-151	Sequence 151, App
38	4313.8	51.5	6328	7	US-11-263-326-152	Sequence 152, App
39	4209.8	50.2	6018	7	US-11-313-450-3	Sequence 3, Appli
40	4042.2	48.2	6003	7	US-11-313-450-5	Sequence 5, Appli
41	3862.4	46.1	6599	7	US-11-263-326-106	Sequence 106, App
42	3862.4	46.1	6599	7	US-11-263-326-107	Sequence 107, App
43	3862.4	46.1	6599	7	US-11-263-326-109	Sequence 109, App
44	3854.4	46.0	6596	7	US-11-263-326-105	Sequence 105, App
45	3508.8	41.9	6371	7	US-11-251-465-8	Sequence 8, Appli

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2006, 22:09:03 ; Search time 23312 Seconds  
 (without alignments)  
 20096.609 Million cell updates/sec

Title: US-10-664-423A-1  
 Perfect score: 8378  
 Sequence: 1 tactgcagaggtctctggtg.....agattacattttttatttta 8378

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : EST:\*  
 1: gb\_est1:\*  
 2: gb\_est3:\*  
 3: gb\_est4:\*  
 4: gb\_est5:\*  
 5: gb\_est6:\*  
 6: gb\_htc:\*  
 7: gb\_est2:\*  
 8: gb\_est7:\*  
 9: gb\_est8:\*  
 10: gb\_est9:\*  
 11: gb\_gss1:\*  
 12: gb\_gss2:\*  
 13: gb\_gss3:\*  
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	IDB	ID	Description
1	5586.8	66.7	5994	14	DQ050103	DQ050103 Homo sapi
2	4739	56.6	5963	14	DQ050104	DQ050104 Pan trogl
3	2447.4	29.2	5943	14	AY416499	AY416499 Homo sapi
4	2227.4	26.6	5710	14	AY416500	AY416500 Pan trogl
5	2110.2	25.2	5666	14	AY416501	AY416501 Mus muscu
6	1937.6	23.1	8452	6	AK147254	AK147254 Mus muscu
7	1937.6	23.1	8452	6	AK147517	AK147517 Mus muscu
8	1856	22.2	4675	6	AK083220	AK083220 Mus muscu

	9	1740	20.8	6096	14	DQ052007	DQ052007 Homo sapi
	10	1514.8	18.1	5751	14	DQ052008	DQ052008 Pan trogl
	11	1450	17.3	5933	6	AK157866	AK157866 Mus muscu
	12	1385.2	16.5	5046	14	DQ042904	DQ042904 Homo sapi
	13	1330.8	15.9	1689	6	AK134744	AK134744 Mus muscu
	14	1182.4	14.1	2222	6	AK032115	AK032115 Mus muscu
	15	1163	13.9	5046	14	DQ042905	DQ042905 Pan trogl
	16	1109	13.2	2306	6	AK141113	AK141113 Mus muscu
	17	961.2	11.5	969	1	AL533359	AL533359 AL533359
	18	933.8	11.1	2802	6	AK032187	AK032187 Mus muscu
	19	903.6	10.8	2527	6	AK158609	AK158609 Mus muscu
	20	866.6	10.3	3043	6	AK148881	AK148881 Mus muscu
	21	787.6	9.4	1762	6	AK142068	AK142068 Mus muscu
c	22	724	8.6	860	9	DN517583	DN517583 1258160 M
	23	717	8.6	853	9	DN520301	DN520301 1263036 M
	24	703.2	8.4	758	5	CJ464951	CJ464951 CJ464951
	25	677.4	8.1	753	5	CJ465757	CJ465757 CJ465757
	26	668.2	8.0	928	3	BQ715936	BQ715936 AGENCOURT
	27	649.2	7.7	683	2	BI667397	BI667397 603292178
	28	647.4	7.7	717	9	DN514870	DN514870 1252030 M
	29	642.2	7.7	840	9	DN875997	DN875997 nae03c06.
c	30	642	7.7	873	8	CN159267	CN159267 948320 MA
c	31	640.2	7.6	1005	1	AL565167	AL565167 AL565167
	32	634.2	7.6	735	2	BI488967	BI488967 603021693
	33	631.8	7.5	672	8	CR750883	CR750883 DKFZp459G
	34	630	7.5	881	12	CC542775	CC542775 CH240_424
	35	610.6	7.3	763	5	CJ465576	CJ465576 CJ465576
	36	609.6	7.3	972	8	CN646516	CN646516 ILLUMIGEN
c	37	608.6	7.3	675	9	DN515541	DN515541 1252798 M
	38	604	7.2	604	9	DA402553	DA402553 DA402553
	39	603.8	7.2	671	9	DA224704	DA224704 DA224704
	40	595.4	7.1	907	8	CN157320	CN157320 946016 MA
	41	594.8	7.1	768	4	CB520657	CB520657 UI-M-GIO-
	42	589.8	7.0	673	8	CR538717	CR538717 DKFZp459P
	43	588.8	7.0	592	4	BX507999	BX507999 DKFZp686B
	44	587	7.0	587	9	DA247582	DA247582 DA247582
	45	585.8	7.0	775	8	CX238600	CX238600 NMA06245